

422 #2



OIKE

RAW SEQUENCE LISTING

DATE: 02/28/2002

PATENT APPLICATION: US/10/016,358

TIME: 10:27:48

Input Set : N:\Cr3\RULE60\10016358.raw.txt

Output Set: N:\CRF3\02282002\J016358.raw

1 <110> APPLICANT: Dixon, Richard A.
 2 Xia, Yiji
 3 Lamb, Christopher
 4 <120> TITLE OF INVENTION: CONSTITUTIVE DISEASE RESISITANCE (CDRI)
 5 GENE AND METHODS OF USE THEREOF
 6 <130> FILE REFERENCE: SALK2820-1
 7 <140> CURRENT APPLICATION NUMBER: 10/016,358
 8 <141> CURRENT FILING DATE: 2001-10-30
 10 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/353,332
 W--> 11 <151> PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-14
 12 <160> NUMBER OF SEQ ID NOS: 3
 13 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 15 <210> SEQ ID NO: 1
 16 <211> LENGTH: 4839
 17 <212> TYPE: DNA
 18 <213> ORGANISM: Arabidopsis thaliana
 19 <220> FEATURE:
 20 <221> NAME/KEY: CDS
 21 <222> LOCATION: (1111)...(2421)
 22 <400> SEQUENCE: 1

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24	ttgagacttt tcaacaaagg gtaatatcgg gaaacctcct cggattccat tgcccagcta	120
25	tctgtcactt catcgaaagg acagtagaaa aggaagatgg cttctacaaa tgccatcatt	180
26	gcgataaagg aaaggctatc gttcaagatg cctctaccga cagtgggtccc aaagatggac	240
27	ccccacccac gaggaacatc gtggaaaaag aagacgttcc aaccacgtct tcaaagcaag	300
28	tggattgatg tgatatcaaa gatgcgagag ttattttatt ttaattgtac tatatttata	360
29	ttgtgatggt tctcttaaat taaaaattta tgactatata tatgacaata tatatatata	420
30	tatatatata tatatacatt attgagatag ataatagaata cattagttaa tcattaaatt	480
31	taatagggtac tgatcttcaa attatttttca aacgattctc tgtcaatttc ttgatatttt	540
32	taaactaaaa tccatttttt aaaaaataga ctgatttaac aaacattaaa agttaattgt	600
33	ttctgtacat gccacggatc gaaaatgagt cagtaaataa atatttttta cctaaagtca	660
34	cacattgtat atacctaagt aaatgatata gaccaaatt agaagatcaa gaatccttat	720
35	attacgaaaa tatccggtta cattcggtga atactttaat gaagaatcta ggatataatt	780
36	aaagaagaag aaaatatgta agcatttaga aataaataa cttggagata taagcaaacc	840
37	ataaacacgt ccatatgaat gaatggtaca ctctctgtaa ataaataaat atatgcatca	900
38	aaatgagaaa atcttcactt ttattttatt ttaatacgtc agattctctg aacacaaaat	960
39	gatataattt gtagataact tactcaaaac gtaagaactc actatctatt atcattttatt	1020
40	aaccaccatc tcattaatct tataaatatg tactcattag attgtcaaaa gtaaacctc	1080
41	acaatacact ttaaactaca aatcaaaaaca atg gcc tct cta ttc tct tca gtt	1134
42	Met Ala Ser Leu Phe Ser Ser Val	
43	1 5	
44	ctc ttg tct ctt tgt tta ctc tct tca ctt ttt ctc tca aat gca aac	1182
45	Leu Leu Ser Leu Cys Leu Leu Ser Ser Leu Phe Leu Ser Asn Ala Asn	

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46	10	15	20	
47	gct aag cca aaa cta ggc ttc acc gcg gat cta atc cac cgt gat tct	1230		
48	Ala Lys Pro Lys Leu Gly Phe Thr Ala Asp Leu Ile His Arg Asp Ser			
49	25 30 35 40			
50	cct aaa tcg ccg ttc tat aac ccg atg gaa acc tct tcc cag cgt cta	1278		
51	Pro Lys Ser Pro Phe Tyr Asn Pro Met Glu Thr Ser Ser Gln Arg Leu			
52	45 50 55			
53	cga aac gcg atc cac cga tcc gtt aac cgt gtt ttc cat ttc act gaa	1326		
54	Arg Asn Ala Ile His Arg Ser Val Asn Arg Val Phe His Phe Thr Glu			
55	60 65 70			
56	aag gat aac aca cca caa cca cag att gac ctc acc tca aat agc ggt	1374		
57	Lys Asp Asn Thr Pro Gln Pro Gln Ile Asp Leu Thr Ser Asn Ser Gly			
58	75 80 85			
59	gaa tat ctc atg aac gta tcc att gga aca cct cct ttc ccg atc atg	1422		
60	Glu Tyr Leu Met Asn Val Ser Ile Gly Thr Pro Pro Phe Pro Ile Met			
61	90 95 100			
62	gcc atc gcc gac acc gga agt gat ctc ctc tgg acg cag tgc gca cca	1470		
63	Ala Ile Ala Asp Thr Gly Ser Asp Leu Leu Trp Thr Gln Cys Ala Pro			
64	105 110 115 120			
65	tgc gat gat tgt tac act caa gtt gat cct ctc ttt gac cct aaa acg	1518		
66	Cys Asp Asp Cys Tyr Thr Gln Val Asp Pro Leu Phe Asp Pro Lys Thr			
67	125 130 135			
68	tct tcc aca tac aaa gac gtt tct tgc tcc tca agt caa tgt act gcc	1566		
69	Ser Ser Thr Tyr Lys Asp Val Ser Cys Ser Ser Ser Gln Cys Thr Ala			
70	140 145 150			
71	cta gaa aat caa gcc tct tgt tcc aca aat gac aac act tgt tct tac	1614		
72	Leu Glu Asn Gln Ala Ser Cys Ser Thr Asn Asp Asn Thr Cys Ser Tyr			
73	155 160 165			
74	tca ttg tct tac ggg gat aac tca tac aca aag ggt aac atc gcc gtg	1662		
75	Ser Leu Ser Tyr Gly Asp Asn Ser Tyr Thr Lys Gly Asn Ile Ala Val			
76	170 175 180			
77	gat acc tta acg ctc ggc tcc agc gat acc cgc cct atg cag ctt aag	1710		
78	Asp Thr Leu Thr Leu Gly Ser Ser Asp Thr Arg Pro Met Gln Leu Lys			
79	185 190 195 200			
80	aat att att atc ggt tgt ggt cac aac aac gct gga acg ttt aac aag	1758		
81	Asn Ile Ile Ile Gly Cys Gly His Asn Asn Ala Gly Thr Phe Asn Lys			
82	205 210 215			
83	aaa ggc tct gga atc gtc gga cta ggt ggt ggt ccg gtt tcg ctt atc	1806		
84	Lys Gly Ser Gly Ile Val Gly Leu Gly Gly Gly Pro Val Ser Leu Ile			
85	220 225 230			
86	aag caa ctt ggc gac tcc atc gac ggt aaa ttc tca tac tgc ttg gtt	1854		
87	Lys Gln Leu Gly Asp Ser Ile Asp Gly Lys Phe Ser Tyr Cys Leu Val			
88	235 240 245			
89	cct cta act tcc aaa aag gat caa acg agt aaa atc aac ttc gga acc	1902		
90	Pro Leu Thr Ser Lys Lys Asp Gln Thr Ser Lys Ile Asn Phe Gly Thr			
91	250 255 260			
92	aat gcc atc gtg tcg gga tca gga gtt gtc tca act cct ctg atc gca	1950		
93	Asn Ala Ile Val Ser Gly Ser Gly Val Val Ser Thr Pro Leu Ile Ala			
94	265 270 275 280			

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95	aag gcg tct caa gag acc ttc tat tac cta acc cta aaa tcc att agc	1998
96	Lys Ala Ser Gln Glu Thr Phe Tyr Tyr Leu Thr Leu Lys Ser Ile Ser	
97	285 290 295	
98	gtg gga agc aag caa atc caa tac tca ggc tca gat tct gaa agc agc	2046
99	Val Gly Ser Lys Gln Ile Gln Tyr Ser Gly Ser Asp Ser Glu Ser Ser	
100	300 305 310	
101	gag gga aac atc atc atc gat tca ggc aca act tta acg tta tta ccg	2094
102	Glu Gly Asn Ile Ile Ile Asp Ser Gly Thr Thr Leu Thr Leu Leu Pro	
103	315 320 325	
104	act gaa ttt tac tcc gag ctc gag gat gcg gtt gca tcc tct atc gat	2142
105	Thr Glu Phe Tyr Ser Glu Leu Glu Asp Ala Val Ala Ser Ser Ile Asp	
106	330 335 340	
107	gct gag aag aag caa gat cca caa agc ggt ttg agt cta tgt tac agt	2190
108	Ala Glu Lys Lys Gln Asp Pro Gln Ser Gly Leu Ser Leu Cys Tyr Ser	
109	345 350 355 360	
110	gca acc gga gat cta aaa gtt cca gtc att act atg cat ttt gat gga	2238
111	Ala Thr Gly Asp Leu Lys Val Pro Val Ile Thr Met His Phe Asp Gly	
112	365 370 375	
113	gcc gat gtg aag ctt gac tcc tcc aat gcc ttt gta caa gtc tgc gag	2286
114	Ala Asp Val Lys Leu Asp Ser Ser Asn Ala Phe Val Gln Val Ser Glu	
115	380 385 390	
116	gat ttg gtt tgc ttt gcc ttc cgc gga agc ccg agt ttc tcc ata tac	2334
117	Asp Leu Val Cys Phe Ala Phe Arg Gly Ser Pro Ser Phe Ser Ile Tyr	
118	395 400 405	
119	ggt aat gtg gcg cag atg aac ttt ctt gtt gga tac gac act gtt tcc	2382
120	Gly Asn Val Ala Gln Met Asn Phe Leu Val Gly Tyr Asp Thr Val Ser	
121	410 415 420	
122	aaa acg gtg tca ttt aag cca aca gat tgt gca aag atg tagttgtttc	2431
123	Lys Thr Val Ser Phe Lys Pro Thr Asp Cys Ala Lys Met	
124	425 430 435	
125	atctcaacat gtttttcaaa attgtgtttt caattacaat aatggctgat ttagttttcag	2491
126	ccttagttct tttgaatttt tctaattcac atgtagtagt ctatcttttc aaggagagat	2551
127	taaattctcg accttttggt cttttggtga tgctttgtat ttctttgaat ttccaatcac	2611
128	aattaaaatc atgaaaacct tatctccggt aactattttc ttgtccatct ctatactctg	2671
129	ttttagttta taatcatctc tatgatgtaa accaaatatg acaagacaat tctataattt	2731
130	tgttcaaaat ttagtttttt ttttcatttt actaataaaa tctagaaata ctacttttgt	2791
131	gtctattata ttattgtgat gaaatactta taagaaacag atgaatgtga ttotaattca	2851
132	atattgcttt taaggaatta tattggtcct actattctat tttgatgtgt totatatttt	2911
133	actatattca atgggattat ggattataga aatattttga aaatattata ctattattta	2971
134	taaataattc aattagtttt tcttcttaag tttcttataa aaaataaata tatcttataa	3031
135	gaaataaata tattttatat ttcataaaaa tcatacattg tacatatcta ggtggatgat	3091
136	acatggccta aattagatca tgaatcataa aaatccagct gtagataaac ataacaagga	3151
137	tgaatggtac aatcctggtc aaaaaaata aaaggaaaag ttatatgcat taaaatgaga	3211
138	aaatcttcgc ttttattggt tcttattttat cagattctct aaatgtaaat gacacaattt	3271
139	gtagataatt tactaaaaat gtaagaatct catcatgtac taccatttat gaatccttat	3331
140	ccaattgacc ttataaatat tactcatcag attgtcaaaa gtaaaaaactg accattcagg	3391
141	caatcactta aactacaatc taagaaaatg gcctctctat tcaacttcaact tctcttgtct	3451
142	ctatgtttat tctcttctcc tattttctca aacgcaaacg ccaaaccaaa actaggcttc	3511
143	accgcggatc tgatccaccg cgattctcct aaatcgccat tctataaccc ggcggaaacc	3571

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144 ccttcccaac gtatgagaaa cgctatccac cgatccttta accgtgcttc ccatttcagt 3631
145 aatctttttg aaaaggatgc atcaactaac gcaccacaaa ctgatatac caaatatttc 3691
146 ggtatatatc ttatgaacgt atcccttggg agttgggaca cctcccgctc caatcatggc 3751
147 ggccgctgac accggaagtg atctcatctg gacgcagtg aaaccatgag atgattgtta 3811
148 cactcaagtt gatcctctct ttgaccctaa agcgtcttcc acatacaaag acgtttcttg 3871
149 cccctcaagc caatgtaggg ctctaaaaga tgatgcttct tgttccaaaa aagacaacac 3931
150 ttgctcttac tcaatgaatt acggggataa ctcaactca cggggtaatg tcgctgtgga 3991
151 taccttaacg ctcggtcca cggataaccg tccggtgcag gttaagaata ttatcatcgg 4051
152 ttgtggtcac gaaaacgctg taacatttag aaacaagagc tctggaatcg ttggacttgg 4111
153 tgggtggtgcg gtttcgctcg ttaaacaact cgggagactcc atcgaaggta aattctcata 4171
154 ctgcttggtg cctgaaaatg atcaaacgag caagattagt ttcggaacca atgcggttgt 4231
155 gtcgggaccg ggaactgtct caactccttt ggctcgtaag tctccagaga ccttctatct 4291
156 tctaacccta aaatctatta cgtggaag caagaatatg ccaaccccag gctctgatat 4351
157 caagggaac atggtcatcg attcgggcac aactctaact ctgttacctg ggaaatatta 4411
158 tttccagatt gagagtgtg ttgctctttt aatcgatgca gagaggctga aagatgaaag 4471
159 aatcggttcg agtctttgat acaatgcaac cgcagatctg aaagtcccag tcattactat 4531
160 gcatttcgat ggagcagatg tgaagcttga ttctataat tcatttttta aagtctcaga 4591
161 tgatttgggt tgctttgcct ttggcttgaa ctgattacg agggatggga tatacgggaa 4651
162 tgtgggcgag aagaactttc ttgttgata cgacactgtt tccaaatcgt tgtcatttaa 4711
163 aaaaacagat tgtgcaaaga ttagatggt tcagcttagc atgtggctaa tttccttttt 4771
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167 <210> SEQ ID NO: 2

168 <211> LENGTH: 437

169 <212> TYPE: PRT

170 <213> ORGANISM: Arabidopsis thaliana

171 <400> SEQUENCE: 2

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175 20 25 30
176 Ala Asp Leu Ile His Arg Asp Ser Pro Lys Ser Pro Phe Tyr Asn Pro
177 35 40 45
178 Met Glu Thr Ser Ser Gln Arg Leu Arg Asn Ala Ile His Arg Ser Val
179 50 55 60
180 Asn Arg Val Phe His Phe Thr Glu Lys Asp Asn Thr Pro Gln Pro Gln
181 65 70 75 80
182 Ile Asp Leu Thr Ser Asn Ser Gly Glu Tyr Leu Met Asn Val Ser Ile
183 85 90 95
184 Gly Thr Pro Pro Phe Pro Ile Met Ala Ile Ala Asp Thr Gly Ser Asp
185 100 105 110
186 Leu Leu Trp Thr Gln Cys Ala Pro Cys Asp Asp Cys Tyr Thr Gln Val
187 115 120 125
188 Asp Pro Leu Phe Asp Pro Lys Thr Ser Ser Thr Tyr Lys Asp Val Ser
189 130 135 140
190 Cys Ser Ser Ser Gln Cys Thr Ala Leu Glu Asn Gln Ala Ser Cys Ser
191 145 150 155 160
192 Thr Asn Asp Asn Thr Cys Ser Tyr Ser Leu Ser Tyr Gly Asp Asn Ser
193 165 170 175

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194 Tyr Thr Lys Gly Asn Ile Ala Val Asp Thr Leu Thr Leu Gly Ser Ser
195           180           185           190
196 Asp Thr Arg Pro Met Gln Leu Lys Asn Ile Ile Ile Gly Cys Gly His
197           195           200           205
198 Asn Asn Ala Gly Thr Phe Asn Lys Lys Gly Ser Gly Ile Val Gly Leu
199           210           215           220
200 Gly Gly Gly Pro Val Ser Leu Ile Lys Gln Leu Gly Asp Ser Ile Asp
201           225           230           235           240
202 Gly Lys Phe Ser Tyr Cys Leu Val Pro Leu Thr Ser Lys Lys Asp Gln
203           245           250           255
204 Thr Ser Lys Ile Asn Phe Gly Thr Asn Ala Ile Val Ser Gly Ser Gly
205           260           265           270
206 Val Val Ser Thr Pro Leu Ile Ala Lys Ala Ser Gln Glu Thr Phe Tyr
207           275           280           285
208 Tyr Leu Thr Leu Lys Ser Ile Ser Val Gly Ser Lys Gln Ile Gln Tyr
209           290           295           300
210 Ser Gly Ser Asp Ser Glu Ser Ser Glu Gly Asn Ile Ile Ile Asp Ser
211           305           310           315           320
212 Gly Thr Thr Leu Thr Leu Leu Pro Thr Glu Phe Tyr Ser Glu Leu Glu
213           325           330           335
214 Asp Ala Val Ala Ser Ser Ile Asp Ala Glu Lys Lys Gln Asp Pro Gln
215           340           345           350
216 Ser Gly Leu Ser Leu Cys Tyr Ser Ala Thr Gly Asp Leu Lys Val Pro
217           355           360           365
218 Val Ile Thr Met His Phe Asp Gly Ala Asp Val Lys Leu Asp Ser Ser
219           370           375           380
220 Asn Ala Phe Val Gln Val Ser Glu Asp Leu Val Cys Phe Ala Phe Arg
221           385           390           395           400
222 Gly Ser Pro Ser Phe Ser Ile Tyr Gly Asn Val Ala Gln Met Asn Phe
223           405           410           415
224 Leu Val Gly Tyr Asp Thr Val Ser Lys Thr Val Ser Phe Lys Pro Thr
225           420           425           430
226 Asp Cys Ala Lys Met
227           435
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230 <211> LENGTH: 14
231 <212> TYPE: PRT
232 <213> ORGANISM: Artificial Sequence
233 <220> FEATURE:
234 <223> OTHER INFORMATION: synthetic peptide utilized for antibody
235 production; segment of SEQ ID NO:2
236 <400> SEQUENCE: 3
237 Asp Thr Val Ser Lys Thr Val Ser Phe Lys Pro Thr Asp Cys
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VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10016358.raw.txt

Output Set: N:\CRF3\02282002\J016358.raw

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